

Search Forms

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## Refine Search

## Search Results -

Terms	Documents
metzker.in. with michael.in.	17

Database:

US Pre-Grant Publication Full-Text Database  
 US Patents Full-Text Database  
 US OCR Full-Text Database  
 EPO Abstracts Database  
 JPO Abstracts Database  
 Derwent World Patents Index  
 IBM Technical Disclosure Bulletins

Search:

L8

Refine Search

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Clear

Interrupt

## Search History

DATE: Wednesday, August 09, 2006 [Printable Copy](#) [Create Case](#)Set Name Query

side by side

Hit Count Set Name

result set

DB=PGPB,USPT; THES=ASSIGNEE; PLUR=YES; OP=AND

<u>L1</u>	KCNQ	149	<u>L1</u>
<u>L2</u>	KCNQ5	73	<u>L2</u>
<u>L3</u>	L1 or L2	171	<u>L3</u>
<u>L4</u>	Petrukhin.in. with konstantin.in.	4	<u>L4</u>
<u>L5</u>	caskey.in. with thomas.in.	16	<u>L5</u>
<u>L6</u>	li.in. with wen.in.	483	<u>L6</u>
<u>L7</u>	L6 and L3	2	<u>L7</u>
<u>L8</u>	metzker.in. with michael.in.	17	<u>L8</u>

END OF SEARCH HISTORY

FILE: 'MEDLINE, BIOSIS, EMBASE, SCISEARCH, CAPLUS' ENTERED AT 15:36:42 ON  
09 AUG 2006

L1 174 S KCNQ5  
L2 80 DUP REM L1 (94 DUPLICATES REMOVED)  
L3 4 S KCNQ-5  
L4 83 S L2 OR L3  
EXPAND PETRUKHIN K/AU  
L5 247 S E3-E8  
L6 1 S L5 AND KCNQ?  
EXPAND CACKEY C/AU  
EXPAND CASKEY C/AU  
L7 1939 S E3, E10-E11, E18-E19  
L8 1 S L7 AND KCNQ?  
L9 6 S L7 AND POTASSIUM CHANNEL  
L10 2 DUP REM L9 (4 DUPLICATES REMOVED)  
EXPAND METZKER M/AU  
L11 209 S E3-E7  
L12 1 S L11 AND POTASSIUM CHANNEL  
L13 1 S L5 AND POTASSIUM CHANNEL

8-9-06 g

STIC Search for SEQ ID NO 2,  
nucleic acids encoding SEQ ID NO 3

Oligo search for SEQ ID NO: 2

SEQ ID NO: 1 1-500  
" " 77251-77751

26951-27451

125410-125910

92501-93001

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2006, 12:57:25 ; Search time 1109 Seconds  
(without alignments)  
5959.400 Million cell updates/sec

Title: US-09-937-499-2  
Perfect score: 3718  
Sequence: 1 ctggagtgaggcgcggggaag.....caaagggcaatgagagggag 3718

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/1\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	3030.2	81.5	3137	3 US-09-590-304-1	Sequence 1, Appli
2	2778.6	74.7	3111	3 US-09-825-147-3	Sequence 3, Appli
3	2744.6	73.8	3074	3 US-09-813-148-1	Sequence 1, Appli
4	2585	69.5	2694	3 US-09-866-020A-1	Sequence 1, Appli
5	2523.2	67.9	2772	3 US-09-825-147-1	Sequence 1, Appli
6	1026	27.6	1090	3 US-09-866-020A-4	Sequence 4, Appli
7	518.4	13.9	2196	3 US-09-949-016-1823	Sequence 1823, Ap
8	518.4	13.9	2335	3 US-09-492-361-1	Sequence 1, Appli
9	511.4	13.8	582	3 US-09-495-050A-303	Sequence 303, App
10	511.4	13.8	2273	3 US-09-177-650-88	Sequence 88, Appl
11	506	13.6	2169	3 US-09-105-058C-22	Sequence 22, Appl
12	465.4	12.5	896	3 US-09-105-058C-1	Sequence 1, Appli
13	460.4	12.4	2814	3 US-09-177-650-90	Sequence 90, Appl
14	455.2	12.2	2565	3 US-09-105-058C-26	Sequence 26, Appl
15	455.2	12.2	2914	3 US-09-177-650-6	Sequence 6, Appli
16	453.6	12.2	575	3 US-09-495-050A-305	Sequence 305, App

17	423	11.4	3287	3	US-09-105-058C-19	Sequence 19, Appl
18	421.4	11.3	900	3	US-09-105-058C-3	Sequence 3, Appli
19	421.4	11.3	3232	3	US-09-177-650-1	Sequence 1, Appli
20	421.4	11.3	3237	3	US-09-177-650-95	Sequence 95, Appl
21	420.6	11.3	900	3	US-09-105-058C-5	Sequence 5, Appli
22	363.8	9.8	930	3	US-09-105-058C-17	Sequence 17, Appl
23	334.2	9.0	735	3	US-09-105-058C-7	Sequence 7, Appli
24	278	7.5	284	3	US-09-495-050A-304	Sequence 304, App
25	267.8	7.2	2028	3	US-09-634-920-1	Sequence 1, Appli
26	267.8	7.2	2028	3	US-09-840-125-1	Sequence 1, Appli
27	267.8	7.2	3181	3	US-09-135-021-1	Sequence 1, Appli
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35	266.6	7.2	2734	3	US-09-135-021-79	Sequence 79, Appl
36	266.6	7.2	2821	3	US-09-135-010A-115	Sequence 115, App
37	266.6	7.2	2821	3	US-09-597-735-115	Sequence 115, App
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39	266.6	7.2	2821	3	US-09-597-731-115	Sequence 115, App
40	266.6	7.2	2924	3	US-09-949-016-32	Sequence 32, Appl
41	258.4	6.9	3182	3	US-09-135-021-5	Sequence 5, Appli
42	251.8	6.8	2633	3	US-09-949-016-3215	Sequence 3215, Ap
43	134.6	3.6	251	3	US-09-495-050A-296	Sequence 296, App
44	95.8	2.6	171	3	US-09-177-650-102	Sequence 102, App
45	95.8	2.6	58543	3	US-09-949-016-13565	Sequence 13565, A

RESULT 9

US-09-495-050A-303

; Sequence 303, Application US/09495050A

: Patent No. 6492505

## : GENERAL INFORMATION:

; APPLICANT: Roopa, Reddy

: APPLICANT: Guegler, Karl, J.

: APPLICANT: Au-Young, Janice

1. TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED PROTE

FILE REFERENCE: PA-0013 US

; CURRENT APPLICATION NUMBER: US/09/495,050A

CURRENT FILING DATE: 2000-01-31

; PRIOR APPLICATION NUMBER: 60/118,318

; PRIOR FILING DATE: February 1, 1999

; NUMBER OF SEQ ID NOS: 305

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; SOFTWARE: PERL Program
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; SEQ ID NO 303

LENGTH: 582

TYPE: DNA

; ORGANISM: Homo sapiens

FEATURE:

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; NAME/KEY: misc feature
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OTHER INFORMATION: Incyte ID No. 6492505 4970006CT1

US-09-495-050A-303

Query Match 13.8%; Score 511.4; DB 3; Length 582;  
Best Local Similarity 99.6%; Pred. No. 7.2e-139;  
Matches 523; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1605 GGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACAGCAGAACATGAG 1664

Db 1 GGAAAAGGGCAAATCAGATCAGATAAGAAGAGCCGAGAGAAAAATAACAGCAGAACATGAG 60

Qv 1665 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1724

Db 61 ACCACAGACGATCTCAGTATGCTCGGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 120

Ov 1725 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1784

Db 121 ATAGAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 180

Qy 1785 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 1844

Db 181 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACCTTTTGAATGTGAACAGACATCT 240

Qy 1845 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC 1904

Db 241 GACTATCAAAGCCCTGTGGATAGCAAAGATCTTTCCGGTTCCGCACAAAAAGTGGCTGC 300

Qy 1905 TTATCCAGATCAACTAGTGCCAACATCTCGAGAGGCCTGCAGTTCATTCTGACGCCAAAT 1964

Db 301 TTATCCAGATCAACTAGTGCCAACTCTCGAGAGGCCTGCAGTTATTCTGACGCCAAAT 360

Qy 1965 GAGTTCAGTGCCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2024

Db 361 GAGTTTCAGTGCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 420

Qy 2025 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 2084

Db 421 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTGCAAACCAA 480

Qy 2085 ATAAATACGGCACCC<sup>1</sup>CAAGCCAGCAGCCCCAACAACTTTACAGATC 2129

Db 481 ATAAATACGGCACCAAGCCAGCAG-CCCAACAACCTTTACAGATC 524

RESULT 69

US-09-258-797-70

; Sequence 70, Application US/09258797

; Patent No. 6183967

; GENERAL INFORMATION:

; APPLICANT: Jayasena, Sumedha

; APPLICANT: Gold, Larry

; TITLE OF INVENTION: Nucleic Acid Ligand Inhibitors to DNA Polymerases

; FILE REFERENCE: NEX 43C/PCT-CIP

; CURRENT APPLICATION NUMBER: US/09/258,797

; CURRENT FILING DATE: 1999-03-01

; EARLIER APPLICATION NUMBER: 08/945,734

; EARLIER FILING DATE: 1997-10-28

; EARLIER APPLICATION NUMBER: 08/487,426

; EARLIER FILING DATE: 1995-06-07

; EARLIER APPLICATION NUMBER: 08/487,720

; EARLIER FILING DATE: 1995-06-07

; EARLIER APPLICATION NUMBER: 08/484,557

; EARLIER FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 119

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 70

; LENGTH: 51

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Sequence

US-09-258-797-70

Query Match 0.5%; Score 18; DB 3; Length 51;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2604 CGATCATCTCAGAGCATT 2621

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Db 9 CGATCATCTCAGAGCATT 26